SEQUENCE LISTING

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<110> The Government of the United States of America, as
<120> MOLECULAR CLONES WITH MUTATED HIV GAG/POL, SIV GAG AND
      SIV ENV GENES
<130> 2026-4287US1 HIV GAG/POL, SIV GAG & ENV
<140> TO BE ASSIGNED
<141> 2001-06-01
<150> PCT/US00/34985
<151> 2000-12-22
<150> 60/173,036
<151> 1999-12-23
<160> 19
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<210> 2 <211> 2507 <212> DNA <213> Human immunodeficiency virus type 1

<400> 2

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<210> 3

<211> 2467

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mutated Human Immunodeficiency Virus - 1 Pol gene

<400> 3

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<210> 4

<211> 1533

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mutated Simian Immunodeficiency Virus Gag gene

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<210> 5

<211> 1532

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
 sequence of mutated Simian Immunodeficiency Virus
 Gag gene (SIVgagDX) with wild-type SIV 239 Gag
 gene

<400> 5

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<210> 6 <211> 8366 <212> DNA <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence
 of the construct pCMVgagpolBNKan containing a CMV
 promoter, a HIV gag/pol gene and a kanamycin
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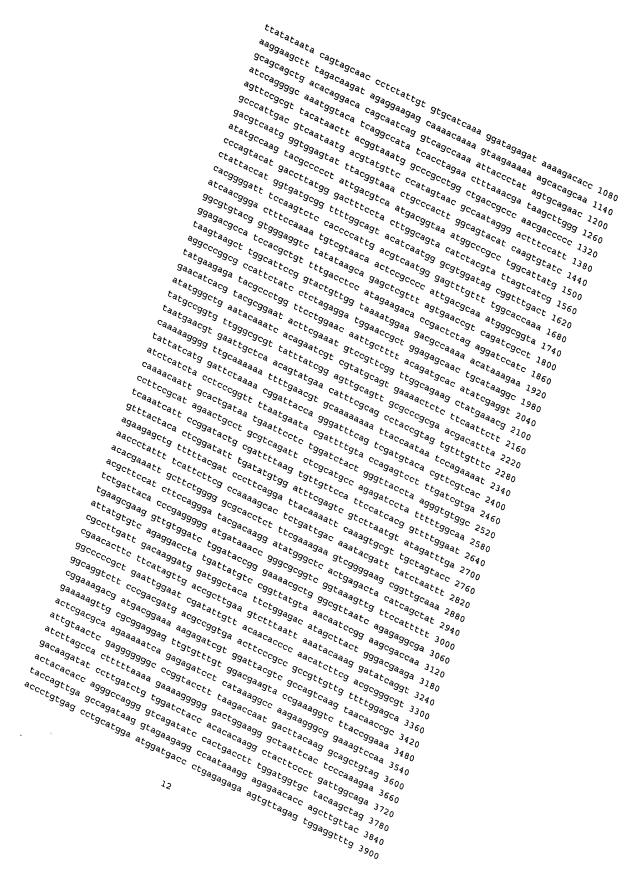
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<212> DNA

<213> Artificial Sequence

<220>

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 construct pmBCwCNluci and pmBCmCNluci

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<211> 122

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence
 of the BSSHII to ClaI fragment in transfer
 construct 3

<400> 11

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<210> 12

<211> 122

<212> DNA

<213> Human immunodeficiency virus type 1

<400> 12

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<213>	Artificial Sequence	
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	Consensus sequence of DNA sequence of the BSSHII	
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aa		.22
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<213>	Artificial Sequence	
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<220>		
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	of construct CMVkan/R-R-SIVgp160 CTE	
<400>	- 14	
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cg	1	122
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<210>	• 15	
<211>	→ 6978	
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	of construct CMVkan/R-R-SIVgp160 CTE	
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Pro Ala Trp Arg Asn Ala Thr Ile Pro Leu Phe Cys Ala Thr Lys Asn 35 40 45

Arg Asp Thr Trp Gly Thr Thr Gln Cys Leu Pro Asp Asn Gly Asp Tyr
50 55 60

Ser Glu Val Ala Leu Asn Val Thr Glu Ser Phe Asp Ala Trp Asn Asn 65 70 75 80

Thr Val Thr Glu Gln Ala Ile Glu Asp Val Trp Gln Leu Phe Glu Thr
85 90 95

Ser Ile Lys Pro Cys Val Lys Leu Ser Pro Leu Cys Ile Thr Met Arg 100 105 110

- Cys Asn Lys Ser Glu Thr Asp Arg Trp Gly Leu Thr Lys Ser Ile Thr
- Thr Thr Ala Ser Thr Thr Ser Thr Thr Ala Ser Ala Lys Val Asp Met 130 135 140
- Val Asn Glu Thr Ser Ser Cys Ile Ala Gln Asp Asn Cys Thr Gly Leu 145 150 155 160
- Glu Gln Glu Gln Met Ile Ser Cys Lys Phe Asn Met Thr Gly Leu Lys 165 170 175
- Arg Asp Lys Lys Glu Tyr Asn Glu Thr Trp Tyr Ser Ala Asp Leu 180 185 190
- Val Cys Glu Gln Gly Asn Asn Thr Gly Asn Glu Ser Arg Cys Tyr Met
 195 200 205
- Asn His Cys Asn Thr Ser Val Ile Gln Glu Ser Cys Asp Lys His Tyr 210 215 220
- Trp Asp Ala Ile Arg Phe Arg Tyr Cys Ala Pro Pro Gly Tyr Ala Leu 225 230 235 240
- Leu Arg Cys Asn Asp Thr Asn Tyr Ser Gly Phe Met Pro Lys Cys Ser 245
- Lys Val Val Ser Ser Cys Thr Arg Met Met Glu Thr Gln Thr Ser
- Thr Trp Phe Gly Phe Asn Gly Thr Arg Ala Glu Asn Arg Thr Tyr Ile 275 280 285
- Tyr Trp His Gly Arg Asp Asn Arg Thr Ile Ile Ser Leu Asn Lys Tyr 290 295 300
- Tyr Asn Leu Thr Met Lys Cys Arg Arg Pro Gly Asn Lys Thr Val Leu 305 310 315 320
- Pro Val Thr Ile Met Ser Gly Leu Val Phe His Ser Gln Pro Ile Asn 325 330 335
- Asp Arg Pro Lys Gln Ala Trp Cys Trp Phe Gly Gly Lys Trp Lys Asp 340 345 350
- Ala Ile Lys Glu Val Lys Gln Thr Ile Val Lys His Pro Arg Tyr Thr 355 360 365

- Gly Thr Asn Asn Thr Asp Lys Ile Asn Leu Thr Ala Pro Gly Gly 370 375 380
- Asp Pro Glu Val Thr Phe Met Trp Thr Asn Cys Arg Gly Glu Phe Leu 385 390 395 400
- Tyr Cys Lys Met Asn Trp Phe Leu Asn Trp Val Glu Asp Arg Asn Thr
 405 410 415
- Ala Asn Gln Lys Pro Lys Glu Gln His Lys Arg Asn Tyr Val Pro Cys
 420 425 430
- His Ile Arg Gln Ile Ile Asn Thr Trp His Lys Val Gly Lys Asn Val
 435
 440
 445
- Tyr Leu Pro Pro Arg Glu Gly Asp Leu Thr Cys Asn Ser Thr Val Thr 450 455 460
- Ser Leu Ile Ala Asn Ile Asp Trp Ile Asp Gly Asn Gln Thr Asn Ile 465 470 475 480
- Thr Met Ser Ala Glu Val Ala Glu Leu Tyr Arg Leu Glu Leu Gly Asp 485 490 495
- Tyr Lys Leu Val Glu Ile Thr Pro Ile Gly Leu Ala Pro Thr Asp Val 500 505 510
- Lys Arg Tyr Thr Thr Gly Gly Thr Ser Arg Asn Lys Arg Gly Val Phe 515 520 525
- Val Leu Gly Phe Leu Gly Phe Leu Ala Thr Ala Gly Ser Ala Met Gly 530 535 540
- Ala Ala Ser Leu Thr Leu Thr Ala Gln Ser Arg Thr Leu Leu Ala Gly 545 550 555 560
- Ile Val Gln Gln Gln Gln Leu Leu Asp Val Val Lys Arg Gln Gln 565 570 575
- Glu Leu Leu Arg Leu Thr Val Trp Gly Thr Lys Asn Leu Gln Thr Arg
 580 585 590
- Val Thr Ala Ile Glu Lys Tyr Leu Lys Asp Gln Ala Gln Leu Asn Ala 595 600 605
- Trp Gly Cys Ala Phe Arg Gln Val Cys His Thr Thr Val Pro Trp Pro 610 615 620

- Asn Ala Ser Leu Thr Pro Lys Trp Asn Asn Glu Thr Trp Gln Glu Trp 625 630 635 640
- Glu Arg Lys Val Asp Phe Leu Glu Glu Asn Ile Thr Ala Leu Leu Glu 645 650 655
- Glu Ala Gln Ile Gln Glu Lys Asn Met Tyr Glu Leu Gln Lys Leu 660 665 670
- Asn Ser Trp Asp Val Phe Gly Asn Trp Phe Asp Leu Ala Ser Trp Ile 675 680 685
- Lys Tyr Ile Gln Tyr Gly Val Tyr Ile Val Val Gly Val Ile Leu Leu 690 695 700
- Arg Ile Val Ile Tyr Ile Val Gln Met Leu Ala Lys Leu Arg Gln Gly 705 710 715 720
- Tyr Arg Pro Val Phe Ser Ser Pro Pro Ser Tyr Phe Gln Gln Thr His
 725 730 735
- Ile Gln Gln Asp Pro Ala Leu Pro Thr Arg Glu Gly Lys Glu Arg Asp
 740 745 750
- Gly Gly Glu Gly Gly Asn Ser Ser Trp Pro Trp Gln Ile Glu Tyr 755 760 765
- Ile His Phe Leu Ile Arg Gln Leu Ile Arg Leu Leu Thr Trp Leu Phe 770 775 780
- Ser Asn Cys Arg Thr Leu Leu Ser Arg Val Tyr Gln Ile Leu Gln Pro 785 790 795 800
- Ile Leu Gln Arg Leu Ser Ala Thr Leu Gln Arg Ile Arg Glu Val Leu 805 810 815
- Arg Thr Glu Leu Thr Tyr Leu Gln Tyr Gly Trp Ser Tyr Phe His Glu 820 825 830
- Ala Val Gln Ala Val Trp Arg Ser Ala Thr Glu Thr Leu Ala Gly Ala 835 840 845
- Trp Gly Asp Leu Trp Glu Thr Leu Arg Arg Gly Gly Arg Trp Ile Leu 850 855 860
- Ala Ile Pro Arg Arg Ile Arg Gln Gly Leu Glu Leu Thr Leu Leu 865 870 875

<210> 17

<211> 271

<212> PRT

<213> Escherichia coli

<400> 17

Met Ser His Ile Gln Arg Glu Thr Ser Cys Ser Arg Pro Arg Leu Asn

Ser Asn Met Asp Ala Asp Leu Tyr Gly Tyr Lys Trp Ala Arg Asp Asn

Val Gly Gln Ser Gly Ala Thr Ile Tyr Arg Leu Tyr Gly Lys Pro Asp

Ala Pro Glu Leu Phe Leu Lys His Gly Lys Gly Ser Val Ala Asn Asp

Val Thr Asp Glu Met Val Arg Leu Asn Trp Leu Thr Glu Phe Met Pro

Leu Pro Thr Ile Lys His Phe Ile Arg Thr Pro Asp Asp Ala Trp Leu

Leu Thr Thr Ala Ile Pro Gly Lys Thr Ala Phe Gln Val Leu Glu Glu

Tyr Pro Asp Ser Gly Glu Asn Ile Val Asp Ala Leu Ala Val Phe Leu

Arg Arg Leu His Ser Ile Pro Val Cys Asn Cys Pro Phe Asn Ser Asp

Arg Val Phe Arg Leu Ala Gln Ala Gln Ser Arg Met Asn Asn Gly Leu

Val Asp Ala Ser Asp Phe Asp Asp Glu Arg Asn Gly Trp Pro Val Glu

Gln Val Trp Lys Glu Met His Lys Leu Leu Pro Phe Ser Pro Asp Ser

Val Val Thr His Gly Asp Phe Ser Leu Asp Asn Leu Ile Phe Asp Glu

Gly Lys Leu Ile Gly Cys Ile Asp Val Gly Arg Val Gly Ile Ala Asp

Arg Tyr Gln Asp Leu Ala Ile Leu Trp Asn Cys Leu Gly Glu Phe Ser 225 230 235

Pro Ser Leu Gln Lys Arg Leu Phe Gln Lys Tyr Gly Ile Asp Asn Pro 245 250 255

Asp Met Asn Lys Leu Gln Phe His Leu Met Leu Asp Glu Phe Phe 260 265 270

<210> 18

<211> 2640

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: DNA sequence of mutated SIV gene in construct CMVkan/R-R-SIVgp160 CTE

<400> 18

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<210> 19 <211> 813 <212> DNA

<213> Escherichia coli

<400> 19

atgagecata tteaaeggga aaegtettge tegaggeege gattaaatte caacatggat 60 getgatttat atgggtataa atgggetege gataatgteg ggeaateagg tgegacaate 120 tategattgt atgggaagee egatgegeea gagttgtte tgaaaeatgg caaaggtage 180 gttgecaatg atgttacaga tgagatggte agactaaaet ggetgaegga atttatgeet 240 etteegacea teaageattt tateegtaet eetgatgatg eatggttaet eaceaetgeg 300 ateeeeggga aaaeageatt eetgagtatta gaagaatate etgatteagg tgaaaatatt 360 gttgatgege tggeagtgtt eetgeeggg ttgeattega teeetgttg taattgteet 420 tttaaeageg ategegtatt tegteteget eaggegeaat eacegaatgaa taaeeggtttg 480 gaaatgeaa agettttga tgaegaget aatgeetgge etgttgaaea agtetggaaa 540 gaaatgeata agettttge eagteegg ateetaegg teaeteatgg tgatteete 600 ettgataace ttatttttga egaggggaaa ttaataggtt gtattgatgt tggaegagte 660 ggaateegaa acegataeea ggatettgee ateetatgga acetgeetegg tgagtttee 720 eetteattae agaaaegget tttteaaaaa tatggtattg ataateetga tatgaataaa 780 ttgeagttte atttgatget egatgagttt tte